

PCF/110
2/18/2002

Serial Number: 10/070,412

CRF Processing Date: 2/18/2002
Edited by: [Signature]
Verified by: [Signature] (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: 1
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☒ Inserted mandatory headings, specifically: Seq. 2
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**



PCT10

RAW SEQUENCE LISTING

DATE: 07/18/2002

PATENT APPLICATION: US/10/070,412

TIME: 21:58:57

Input Set : N:\Crf3\07152002\J070412.raw

Output Set: N:\CRF3\07182002\J070412.raw

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1 <110> APPLICANT: AstaCarotene AB
2 <120> TITLE OF INVENTION: DNA construct and its use
3 <130> FILE REFERENCE: 29295-AstaCarotene
4 <140> CURRENT APPLICATION NUMBER: US/10/070,412
5 <141> CURRENT FILING DATE: 2002-06-12
6 <160> NUMBER OF SEQ ID NOS: 2
7 <170> SOFTWARE: PatentIn Ver. 2.1
9 <210> SEQ ID NO: 1
10 <211> LENGTH: 2543
11 <212> TYPE: DNA
12 <213> ORGANISM: Artificial Sequence
13 <220> FEATURE:
14 <223> OTHER INFORMATION: Description of Artificial Sequence: napin promoter
15 + chloroplast localization signal + beta-carotene C-4 oxygenase
16 coding sequence + termination sequence
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18 <221> NAME/KEY: promoter
19 <222> LOCATION: (1)..(1145)
20 <220> FEATURE:
21 <221> NAME/KEY: transit_peptide
22 <222> LOCATION: (1179)..(1347)
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1179)..(2217)
26 <220> FEATURE:
27 <221> NAME/KEY: terminator
28 <222> LOCATION: (2273)..(2536)
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32 tttccaacat tttaaatttc actattggct gaatgcttct tctttgagga agaaacaatt 180
33 cagatggcag aaatgtatca accaatgcat atatacaaat gtacctcttg ttctcaaaac 240
34 atctatcgga tggttccatt tgctttgtca tccaattagt gactacttta tattattcac 300
35 tcctctttat tactattttc atgcgagggt gccatgtaca ttatatttgt aaggattgac 360
36 gctattgagc gtttttcttc aattttcttt attttagaca tgggtatgaa atgtgtgtta 420
37 gagttgggtt gaatgagata tacgttcaag tgaagtggca taccgttctc gagtaaggat 480
38 gacctacca ttcttgagac aaatgttaca ttttagtatac agagtataat gtgtacctat 540
39 aactcaaatt cgattgacat gtatccattc aacataaaat taaaccagcc tgcacctgca 600
40 tccacatttc aagtattttc aaaccgttcg gctcctatcc accgggtgta acaagacgga 660
41 ttccgaattt ggaagatttt gactcaaatt cccaatttat attgaccgtg actaaatcaa 720
42 ctttaacttc tataattctg attaagctcc caatttatat tcccaacggc actacctcca 780
43 aaatttatag actctcatcc ctttttaaac caacttagta aacgtttttt tttttaattt 840
44 tatgaagtta agtttttacc ttgtttttaa aaagaatcgt tcataagatg ccatgccaga 900

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46  gtcactccct tcaaacacct aagagcttct ctctcacagc acacacatac aatcacatgc 1020
47  gtgcatgcat tattacacgt gatcgccatg caaatctcct ttatagccta taaattaact 1080
48  catccgcttc actctttact caaaccaaaa ctcatacaata caaacaagat taaaaacata 1140
49  cacgaggatc ctcagtcaca caaagagtaa agaagaaca atg gct tcc tct atg 1194
50                                     Met Ala Ser Ser Met
51                                     1 5
52  ctc tct tcc gct act atg gtt gcc tct ccg gct cag gcc act atg gtc 1242
53  Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala Gln Ala Thr Met Val
54                                     10 15 20
55  gct cct ttc aac gga ctt aag tcc tcc gct gcc ttc cca gcc acc cgc 1290
56  Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala Phe Pro Ala Thr Arg
57                                     25 30 35
58  aag gct aac aac gac att act tcc atc aca agc aac ggc gga cgc gtt 1338
59  Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser Asn Gly Gly Arg Val
60                                     40 45 50
61  aac tgc atg tct aga atg cca tcc gag tcg tca gac gca gct cgt cct 1386
62  Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro
63                                     55 60 65
64  gcg cta aag cac gcc tac aaa cct cca gca tct gac gcc aag ggc atc 1434
65  Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile
66                                     70 75 80 85
67  acg atg gcg ctg acc atc att ggc acc tgg acc gca gtg ttt tta cac 1482
68  Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His
69                                     90 95 100
70  gca ata ttt caa atc agg cta ccg aca tcc atg gac cag ctt cac tgg 1530
71  Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp
72                                     105 110 115
73  ttg cct gtg tcc gaa gcc aca gcc cag ctt ttg ggc gga agc agc agc 1578
74  Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser
75                                     120 125 130
76  cta ctg cac atc gct gca gtc ttc att gta ctt gag ttc ctg tac act 1626
77  Leu Leu His Ile Ala Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr
78                                     135 140 145
79  ggt cta ttc atc acc aca cat gac gca atg cat ggc acc ata gct ttg 1674
80  Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Leu
81                                     150 155 160 165
82  agg cac agg cag ctc aat gat ctc ctt ggc aac atc tgc ata tca ctg 1722
83  Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu
84                                     170 175 180
85  tac gcc tgg ttt gac tac agc atg ctg cat cgc aag cac tgg gag cac 1770
86  Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg Lys His Trp Glu His
87                                     185 190 195
88  cac aac cat act ggc gaa gtg ggg aaa gac cct gac ttc cac aag gga 1818
89  His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly
90                                     200 205 210
91  aat ccc ggc ctt gtc ccc tgg ttc gcc agc ttc atg tcc agc tac atg 1866
92  Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met
93                                     215 220 225

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94      tcc ctg tgg cag ttt gcc cgg ctg gca tgg tgg gca gtg gtg atg caa      1914
95      Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln
96      230                      235                      240                      245
97      atg ctg ggg gcg ccc atg gca aat ctc cta gtc ttc atg gct gca gcc      1962
98      Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala
99                      250                      255                      260
100     cca atc ttg tca gca ttc cgc ctc ttc tac ttc ggc act tac ctg cca      2010
101     Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro
102                      265                      270                      275
103     cac aag cct gag cca ggc cct gca gca ggc tct cag gtg atg gcc tgg      2058
104     His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp
105                      280                      285                      290
106     ttc agg gcc aag aca agt gag gca tct gat gtg atg agt ttc ctg aca      2106
107     Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr
108                      295                      300                      305
109     tgc tac cac ttt gac ctg cac tgg gag cac cac aga tgg ccc ttt gcc      2154
110     Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala
111     310                      315                      320                      325
112     ccc tgg tgg cag ctg ccc cac tgc cgc cgc ctg tcc ggg cgt ggc ctg      2202
113     Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu
114                      330                      335                      340
115     gtg cct gcc ttg gca tgacctggtc cctccgctgg tgaccagcg tctgcacaag      2257
116     Val Pro Ala Leu Ala
117                      345
118     agtgtcatgg agctcgaatt tccccgatcg ttcaaacatt tggcaataaa gtttcttaag 2317
119     attgaatcct gttgccggtc ttgcgatgat tatcatataa tttctgttga attacgttaa 2377
120     gcatgtaata attaacatgt aatgcatgac gttatttatg agatgggttt ttatgattag 2437
121     agtcccgcga ttatacattt aatacgcgat agaaaacaaa atatagcgcg caaactagga 2497
122     taaattatcg cgcgcggtgt catctatggt actagatcgg gaattc      2543
124 <210> SEQ ID NO: 2
125 <211> LENGTH: 346
126 <212> TYPE: PRT
127 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: deduced fusion
130     protein of transit peptide + peptide with beta-carotene C-4 oxygenase
131     activity
132 <400> SEQUENCE: 2
133     Met Ala Ser Ser Met Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala
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136     20                      25                      30
137     Phe Pro Ala Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
138     35                      40                      45
139     Asn Gly Gly Arg Val Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser
140     50                      55                      60
141     Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser
142     65                      70                      75                      80
143     Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr

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144					85				90				95
145	Ala	Val	Phe	Leu	His	Ala	Ile	Phe	Gln	Ile	Arg	Leu	Pro
146				100					105				110
147	Asp	Gln	Leu	His	Trp	Leu	Pro	Val	Ser	Glu	Ala	Thr	Ala
148			115					120				125	
149	Gly	Gly	Ser	Ser	Ser	Leu	Leu	His	Ile	Ala	Ala	Val	Phe
150		130					135					140	
151	Glu	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Thr	His	Asp
152		145				150					155		160
153	Gly	Thr	Ile	Ala	Leu	Arg	His	Arg	Gln	Leu	Asn	Asp	Leu
154				165					170				175
155	Ile	Cys	Ile	Ser	Leu	Tyr	Ala	Trp	Phe	Asp	Tyr	Ser	Met
156			180						185				190
157	Lys	His	Trp	Glu	His	His	Asn	His	Thr	Gly	Glu	Val	Gly
158		195					200					205	
159	Asp	Phe	His	Lys	Gly	Asn	Pro	Gly	Leu	Val	Pro	Trp	Phe
160		210				215						220	
161	Met	Ser	Ser	Tyr	Met	Ser	Leu	Trp	Gln	Phe	Ala	Arg	Leu
162		225			230					235			240
163	Ala	Val	Val	Met	Gln	Met	Leu	Gly	Ala	Pro	Met	Ala	Asn
164				245					250				255
165	Phe	Met	Ala	Ala	Ala	Pro	Ile	Leu	Ser	Ala	Phe	Arg	Leu
166			260					265					270
167	Gly	Thr	Tyr	Leu	Pro	His	Lys	Pro	Glu	Pro	Gly	Pro	Ala
168		275					280					285	
169	Gln	Val	Met	Ala	Trp	Phe	Arg	Ala	Lys	Thr	Ser	Glu	Ala
170		290				295					300		
171	Met	Ser	Phe	Leu	Thr	Cys	Tyr	His	Phe	Asp	Leu	His	Trp
172		305				310				315			320
173	Arg	Trp	Pro	Phe	Ala	Pro	Trp	Trp	Gln	Leu	Pro	His	Cys
174				325					330				335
175	Ser	Gly	Arg	Gly	Leu	Val	Pro	Ala	Leu	Ala			
176				340					345				

VERIFICATION SUMMARY

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Input Set : N:\Crf3\07152002\J070412.raw

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